

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 Att Unit _____ Phone Number 30 _____ Serial Number _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number*

BEST AVAILABLE COPY

STAFF USE ONLY

Searcher: P. Schreiber
 Searcher Phone #: 308-4292
 Searcher Location: CMC C103
 Date: 10/8
 Searcher Prep Time: 13
 Searcher Prep Time: 16

Type of Search

NA Sequence (F) _____ STN _____
 AA Sequence (F) 2 _____
 Structure (F) _____
 Bibliographic _____
 Citation _____
 Full text _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

Dialog _____
 Quest _____
 JASIS _____
 Sequences Systems CompuGen GCG
 NIA/NIH Internet ✓
 Other _____

Schreiber, David

105875

From: Ramirez, Delia
Sent: Wednesday, October 08, 2003 3:01 PM
To: Schreiber, David
Subject: case 09/856679

Hi David,

I was wondering if you could do the following alignment. I need baa04770 gi474982 April 27, 1994 against seq id 2 and the corresponding DNA against seq id 31.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, 10D06, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 An Unit _____ Phone Number 30 _____ Serial Number _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number*

BEST AVAILABLE COPY

STAFF USE ONLY

Searcher: P. Schreiber
 Searcher Phone #: 308-4292
 Searcher Location: CM 6A03
 Date: 10/8
 Searcher Priority Filing Time: 12
 Searcher Priority Filing Time: 13

Type of Search

NA Sequence #: 2
 AA Sequence #: 2
 Structure (H): _____
 Bibliographic: _____
 Litigation: _____
 Full-text: _____
 Patent Family: _____
 Other: _____

Vendors and cost where applicable

STN: _____
 Dialog: _____
 Quick: _____
 Compaq: _____
 Compaq: _____
 Compaq: _____
 Compaq: _____
 Compaq: _____

Schreiber, David

5874

From: Ramirez, Delia
Sent: Wednesday, October 08, 2003 5:29 PM
To: Schreiber, David
Subject: case 09/856,679

Hi David,

I would like to request the following alignments:

AC004241 gi 2920325 Feb 1998 against seq id 31
AC004241 gi 3282154 July 1998 against seq id 31
AC004241 gi 3108007 May 2 1998 against seq id 31
AC004241 gi 3046263 Apr 13 1998 against seq id 31
AC004241 gi 3023023 Apr 4 1998 against seq id 31
AC004241 gi 3004524 Apr 1 1998 against seq id 31
AC004241 gi 2995474 Mar 28 1998 against seq id 31
AC004241 gi 2980958 Mar 21 1998 against seq id 31
AC004241 gi 2960506 Mar 14 1998 against seq id 31
AC004241 gi 2943840 Mar 7 1998 against seq id 31

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, 10D06, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2003, 15:50:09 ; Search time 0.001 Seconds
(without alignments)
364.026 Million cell updates/sec

Title: us-09-856-679-2

Perfect score: 1759
Sequence: 1 MALAAGEDGWTGKGVLYKVN.....QLKVIDNQRELRLSLRELPEP 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1077 residues
Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : 474982:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	16.1	1077	1 474982	ACCESSION:474982

ALIGNMENTS

RESULT 1

LOCUS 474982 1077 aa linear 27-APR-1994
DEFINITION C3G protein.
ACCESSION 474982

VERSION GI:474982
DBSOURCE locus HDMC3GP accession D21239

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (residues 1 to 1077)

AUTHORS Tanaka,S.
JOURNAL Unpublished (1994)
COMMENT Submitted (20-Oct-1993) to DDBJ by: Michiyuki Matsuda
1-23-1 Toyama, Shinku-ku
Tokyo 162

Japan
Phone: 03-5285-1111 x2625
Fax: 03-5285-1150.

FEATURES
source Location/Qualifiers

Protein 1..1077
/organism="unknown"

CDS
/product="C3G protein"
/function="ras guanine nucleotide releasing factor"
1..1077

/coded_by="D21239:131..3364"

Query Match 16.1% Score 283; DB 1; Length 1077;
Best Local Similarity 28.3% Pred. No. 0;
Matches 79; Conservative 48; Mismatches 98; Indels 54; Gaps 8;

QY	25	AIGLOP-DARGVATSLGLNERLFVNFQEVHELIPHPDQGPVYGSAGGLDVSANDLAG 83
DB	818	ATSSQPLARGVA-----ARPGTLHDFRSH-----EIAE 846
QY	84	QLTDHDKSLFNSIHQVELIHYVGLPOHLRDVVTANLEFRMRRENELOYWATELCLCPV 143
DB	847	QLTLDAELF---YKIRIPVLLMAKQONEKSPNLTQTFEHFNMSYVWRSIIMLEKA 903
QY	144	GPAQLRFRFKLAHLKEQKNLSFPAVWFGLSNSAISRLAHTWERLPHKVKRLYSALE 203
DB	904	QDRERLTLKFKIKMLKLNFNFSYDAIISALDSAPIRRL--EMOKQTSGLAEYCT-- 959
QY	204	RLDPSWNRVYRLALAKLSPPVIFPMLLLKDMTFIHGNTLVENMLNFER----- 256
DB	960	-LIDSSSFRAVRAALSEVEPFCIPYIGLIDLTFFVHLGNPDYIDCKVAFSKRMQOFNI 10
QY	257	---MRMARAARMLHCRSHNPVPLSPLRERSVSHLED 292
DB	1019	LDWMRCFOQA---HYDMRRNDIINFNFSDHLEEA 1053

Search completed: October 8, 2003, 15:50:09
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 15:55:38 ; Search time 5 Seconds
(without alignments)
3.963 Million cell updates/sec

Title: us-09-856-679-31
Perfect score: 2434
Sequence: 1 caagatccagatggtatata.....cacacacagaaaaaaaaa 2434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 4070 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : d21239.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	90.9001	3.7	4070	1	HUMC3GP ACCESSION:D21239

ALIGNMENTS

RESULT 1
HUMC3GP 4070 bp mRNA linear PRI 19-JUN-1999
DEFINITION Homo sapiens mRNA for C3G protein, complete cds.
ACCESSION D21239
VERSION D21239.1 GI:474981
KEYWORDS C3G protein; CRK SH3-binding protein; GMRP; ras guanine nucleotide releasing factor.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Tanaka,S., Morishita,T., Hashimoto,Y., Hattori,S., Nakamura,S., Shibusawa,M., Matsuda,K., Takekawa,T., Kurata,T., Nagashima,K., and Matsuda,M.

TITLE

C3G, a guanine nucleotide-releasing protein expressed ubiquitously, binds to the Src homology 3 domains of CRK and GRB2/ASH proteins

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3443-3447 (1994)

MEDLINE

94211860
7512734

REFERENCE

AUTHORS Knudsen,B.S., Feller,S.M., and Hanafusa,H.
TITLE Four proline-rich sequences of the guanine-nucleotide exchange factor C3G bind with unique specificity to the first Src homology 3 domain of Crk

J. Biol. Chem. 269 (52), 32781-32787 (1994)

MEDLINE 95105157
PUBMED 7806500
COMMENT Submitted (20-Oct-1993) to DDBJ by:
Michiyuki Matsuda
1-23-1 Toyama, Shinkuku-ku
Tokyo 162
Japan
Phone: 03-5285-1111 x2625
Fax: 03-5285-1150.

FEATURES
SOURCE Location/Qualifiers
1..4070
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pc3g2"
/tissue_type="spleen and placenta"
131..3364
/function="ras guanine nucleotide releasing factor"
/note="1897-2047 bp: binding site for SH3 domains of CRK and GRB2/ASH protein.
2630-3322 bp: guanine nucleotide releasing factor:
homologous region to CDC25"
/codon_start=1
/product="C3G protein"
/protein_id="BA04770.1"
/db_xref="GI:474982"
/translation="MDRDSORSHLSFTMKLMDFHSPKIKRPPSKKGAPEVSKIP
EKPVKREKATDRFLPEGYPLDLEDOAVPEMSTSAVARSOROKNLSMLEKEKSVS
ALRYFKTIVDMKATDKVLEMLPSASKVLEAILPLVONDRIDSHSLSKSRVQ
SLANLIRMSDQVMLEGVNSDEKEMVTVTKGIRKAVLDGVELEVTLEKGRSPIS
VNDSPSPALPKKROGASPTRYAVAVAPMSRATSGSLPVGIRNODPVCYKQRL
SGGSHYSGDESPRLSPCSIDKLSDEOLSLDRSGCSRTCTLDHYDVEF
LQDLISNADQIPQOTAWNISPLPSLESGSPFGPPFOLPIGGHPQDPLAGQOT
DTPPALPEKRRNSAOTADSGCGRYVERRPSYDNISEDDOSTPISVYAPAPA
AILPFOHGSAPVEFVGDFTAPESTDPERPPLEPKKNHMLATVQLLEDISEDP
SMFYQTPQNEHITVOOKNKLMEVGFSDSESGVDSVQELAPPALPKQHOLEPSPACK
DGHPRDPSAVSGPKDSRDGSEAPKSPDLESAQSEEEVDELSTLDHNEIMSRLL
KQEGDDPDVAGSGDILLVATETDRKDLVCEAVLTTRTPISPEELIKLQVRY
EKSPFADPTFRKRYSKNPFYLVVVDLCLVELTEELIKLMLVRLVRLVNGELSLA
RVLEKNLIDKVDOKKILRCATSSQPLAARGVAAAPGLPHPSHEINBOUILLDAEFL
KILPEVLMANQONEKSNLQTEHFNKSYWRSIIMDEKQDRRLKRT
KIMKHLRLNNNSYLA1LSDLSAP1RRLQWQVNSGLAEVCTLLDISSSFAYRA
ALSEVEPCIPYIGLILQDLTFVHIGNDYIDGVNSKRNQOENIUDSMSCFOAHY
DMRRNDIINFNFSDHILAEALMELSLIKRPNIRTRKTDREKRT"

CDS

BASE COUNT 939 a 1197 c 1148 g 786 t

Query Match 3.7%; Score 90.9001; DB 1; Length 4070;
Best Local Similarity 52.8%; Pred. No. 0;
Matches 236; Conservative 0; Mismatches 196; Indels 15; Gaps

QY	1380	TCCACGAGGTCGATATCCACATATGCTGGGCCCCCAGCATCGGGATGACCA	1439
DB	2697	TCTATAAATAGAGATTCCTGAGGTTTGTGGGCAAAAGACAGAGATAGAGAGA	2756
QY	1440	CCGCCAAGCTGAGCGCTTCATGCGCGCTTCAATGAGCTTCAGTACTGGTGCACCG	1499
DB	2757	GCCCCAAGTACACCGAGTTCACGGAGCACTTCAACACATCTCTAGTGGTCCGGTCA	2816
QY	1500	AGCTGTGCTTGTGCCCGCTGCGCGCCCGCCGACAGTCTCTAGCAAGTTCAATGAC	1559
DB	2817	TAAATCATGTTTACAGGAAAGGCGCCAGACAGGAGGAAAGCGCTCTTGAAGTTCA	2876
QY	1560	TGGGGGCGCCACCTCAGAGGAGAGAAATCTCAATTCCTTTGGCGCTATGTTGGCG	1619
DB	2877	TCAATGAGCATTTGGGAGAGCTGAAATCACTTCACTTACTTGGCATCTCTCTGCGC	2936
QY	1620	TCAGCAACTCGGCATCAGCCGCTAGCCACACCTGGAGAGCGCTGCTCACAAGTCC	1679
DB	2937	TGGAAGTGGGGCCGATCGGAGCTGG-----AGTGCANAAACAGACTTCAAGAGGCG	2990
QY	1680	GGAAGCTTACTCCGCGCTCGAGAGGCTGCTGATCCCTCATGGAACACCGGGTATGCC	1739

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2003, 08:57:20 ; Search time 0.001 Seconds
(without alignments)
298.792 Million cell updates/sec

Title: us-09-856-679-2

Perfect score: 1759
Sequence: 1 MALAODGWTGQVLVKVN.....QLKVIDNQRELRLSRELEP 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 884 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database: 4079657.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1664	94.6	884	1	AAD12739 ACCESSION: AAD12739

ALIGNMENTS

RESULT 1
AAD12739 884 aa linear ROD 05-FEB-1999
LOCUS CAMP-regulated guanine nucleotide exchange factor 1 [Rattus
norvegicus].
ACCESSION AAD12739
VERSION AAD12739.1 GI:4079657
DBSOURCE locus RNU78167 accession U78167.1
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (residues 1 to 884)
AUTHORS Kawaasaki, H., Springlett, G. M., Mochizuki, N., Toki, S., Nakaya, M.,
Matsuda, M., Housman, D. E. and Graybiel, A. M.
TITLE A family of CAMP-binding proteins that directly activate Rap1
JOURNAL Science 282 (5397), 2275-2279 (1998)
MEDLINE 99074384
PUBMED 9856955
REFERENCE 2 (residues 1 to 884)
AUTHORS Kawaasaki, H., Housman, D. E. and Graybiel, A. M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-1996) Center for Cancer Research/Department of
Brain and Cognitive Sciences, Massachusetts Institute of
Technology, 77 Massachusetts Avenue, E17-540, Cambridge, MA 02135.

FEATURES

location/Qualifiers

1..884

source /organism="Rattus norvegicus"

/db_xref="taxon:10116"

Protein

1..884 /product="CAMP-regulated guanine nucleotide exchange
factor 1"

CDS

1..884

/gene="CAMP-GEF1"
/coded_by="U78167.1:197..2851"
/note="GEF domain shows highest similarity to RasGEF
family; contains CAMP binding domain"

Query Match 94.6% Score 1664; DB 1; Length 884;

Best Local Similarity 93.5% Pred. No. 0;
Matches 316; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY	1	MAALAODGWTGQVLVKVNSAGDAIGLPDARGVATSLGNERLFPVNPQEVHELIRHP	60
DB	547	MAALAHEDHWTGQVLVKVNSAGDVVGLQPDARGVATSLGNERIRFVVDPEVHELIRHP	60
QY	61	DOLGPTVGSAGGLDYSAKDLAQDLDDHDSLNSTHQVLEIHYVGLPQHLRDVTTANLE	120
DB	607	EQLGPTLGSSEMLDLVSADKDLAQDLDEHDNLFNRHQVELIHYVGLPQHLRDVTTANLE	666
QY	121	RFMRRENELOVWVATELCLCPVPGPRAQLRKFIKLAHLKEOKNLSPFAVMEGLNSNA	180
DB	667	RFMRRENELOVWVATELCLCPVPGPRAQLRKFIKLAHLKEOKNLSPFAVMEGLNSNA	726
QY	181	ISRLAHTWERLPHKVRKLYSALERLLDPSNHNHRYRLALAKLSPPVTFPMPLLLKDTFI	240
DB	727	ISRLAHTWERLPHKVRKLYSALERLLDPSNHNHRYRLALAKLSPPVTFPMPLLLKDTFI	786
QY	241	HEGNHTLVENLINFEEKRMARARARMLHRCRSINPVLSTLRKRVSHLHDSOVARSTC	300
DB	787	HEGNHTLVENLINFEEKRMARARARMLHRCRSINPVLSTLRKRVSHLHDSOVARSTC	846
QY	301	SEQSLSTRSPASTWAVYQQLKVIDNQRELRLSRELEP	338
DB	847	SEQSLSTRSPASTWAVYQQLKVIDNQRELRLSRELEP	884

Search completed: October 8, 2003, 08:57:21
Job time: 1 sec